

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2003, 15:50:54 ; Search time 2343.67 Seconds
(without alignments)
16465.781 Million cell updates/sec

Title: US-09-497-967-1

Perfect score: 1326

Sequence: 1 atgaataataattttatt.....ttattttcttctattttattg 1326

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_on:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_ov:*

22: em_pat:*

23: em_ph:*

24: em_pl:*

25: em_ro:*

26: em_sts:*

27: em_un:*

28: em_vl:*

29: em_vt:*

30: em_htg_hum:*

31: em_htg_in:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1326	100.0	2486	3	AF140273	AF140273 Ichthyoph
2	1170.4	88.3	1249	3	ICVIMANT	M92907 Ichthyoph
3	647.2	48.8	1520	3	AF405431	AF405431 Ichthyoph
4	252.6	19.0	3026	3	AF324424	AF324424 Ichthyoph
C 5	94	7.1	131274	2	AC096869	AC096869 Rattus no
C 6	94	7.1	132449	9	AL365272	AL365272 Human DNA
C 7	94	7.1	176822	2	AC099174	AC099174 Rattus no
C 8	93	7.0	179553	2	AC024253	AC024253 Homo sapi
C 9	89.8	6.8	170985	2	AC096032	AC096032 Rattus no
C 10	88.8	6.7	186935	2	AC022322	AC022322 Homo sapi
C 11	88.4	6.7	189461	2	AC119627	AC119627 Rattus no
C 12	88.4	6.7	191841	2	AC121374	AC121374 Rattus no
C 13	87.6	6.6	204259	2	AC110817	AC110817 Mus muscu
C 14	87.6	6.6	264522	2	AC090437	AC090437 Mus muscu
C 15	86.2	6.5	84472	2	AC096684	AC096684 Takifugu
C 16	83.8	6.3	1611	10	MMU70651	U70651 Mus musculu
C 17	82.6	6.2	172307	2	AC044842	AC044842 Homo sapi
C 18	82.6	6.2	201470	2	AC113649	AC113649 Rattus no
C 19	82.4	6.2	149228	2	AC113774	AC113774 Rattus no
C 20	82.4	6.2	261604	2	AC119819	AC119819 Rattus no
C 21	82.2	6.2	165318	2	AC126747	AC126747 Rattus no
C 22	81.8	6.2	175699	2	AC129136	AC129136 Rattus no
C 23	81.6	6.2	131346	2	AC119558	AC119558 Rattus no
C 24	80	6.0	88203	5	AC097628	AC097628 Takifugu
C 25	79.4	6.0	176774	2	AC109366	AC109366 Rattus no
C 26	79	5.9	209973	2	AC073755	AC073755 Mus muscu
C 27	78.2	5.9	71553	2	AC096997	AC096997 Takifugu
C 28	78.2	5.9	175748	2	AC120669	AC120669 Rattus no
C 29	78.2	5.9	180903	2	AC125859	AC125859 Rattus no
C 30	77.4	5.8	1612	10	MMU70652	U70652 Mus musculu
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C 32	77.2	5.8	85786	9	AL162582	AL162582 Human DNA
C 33	77	5.8	186380	9	AC100822	AC100822 Homo sapi
C 34	76.6	5.8	173540	2	AC119697	AC119697 Rattus no
C 35	76.6	5.8	180668	2	AC020857	AC020857 Mus muscu
C 36	76.2	5.7	183413	2	AC131200	AC131200 Rattus no
C 37	76	5.7	168757	2	AC127508	AC127508 Homo sapi
C 38	75.6	5.7	87201	9	AC007623	AC007623 Homo sapi
C 39	75.4	5.7	172853	9	AC084361	AC084361 Homo sapi
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C 41	75.2	5.7	186558	2	AC079031	AC079031 Homo sapi
C 42	75	5.7	216977	2	AC105611	AC105611 Rattus no
C 43	75	5.7	219761	2	AC105642	AC105642 Rattus no
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Ichthyophthirius multifiliis 2486 bp DNA linear INV 19-MAY-1999
(TAG48) gene, complete cds.
ACCESSION AF140273
VERSION AF140273.1 GI:4868370
KEYWORDS
SOURCE Ichthyophthirius multifiliis.
ORGANISM Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE
AUTHORS 1 (bases 1 to 2486)
Clark,T.G., Lin,T.L., Jackwood,D.A., Sherrill,J., Lin,Y. and
Dickerson,H.W.

TITLE The gene for an abundant parasite coat protein predicts tandemly
 repetitive metal binding domains
 JOURNAL Gene 229 (1-2), 91-100 (1999)
 MEDLINE 99196987
 PubMed 10095108
 REFERENCE 2 (bases 1 to 2486)
 Gaertig,J., Gao,Y., Tishgarten,T., Clark,T.G. and Dickerson,H.W.
 Surface display of a parasite antigen in the ciliate Tetrahymena
 thermophila
 Nat. Biotechnol. (1999) In press
 JOURNAL 3 (bases 1 to 2486)
 Clark,T.G., Lin,T.-L., Jackwood,D.A. and Dickerson,H.W.
 Direct Submission
 Submitted (29-MAR-1999) Microbiology & Immunology, Cornell
 University, College of Veterinary Medicine, Ithaca, NY 14853, USA
 Location/Qualifiers
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 mat_peptide
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 Best Local Similarity 100.0%; Pred. No. 6,1e-241;
 Matches 1326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 433 ATGAATATATATTTTATTAATTTATTTCTTTTATTTATTTAATGAATAGAGCT 492
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 QY 181 GAAGCTAATGTTAATTAACCTTCGACGAGAAATATGCTGCTAGAGGTATATGCTTACCA 240
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 QY 241 TGCCAAATAAACAAGTAGGCTCTGTTACCAATGCAGGTGACTTAGCTACTTTAGCCACA 300
 DB 673 TGCCAAATAAACAAGTAGGCTCTGTTACCAATGCAGGTGACTTAGCTACTTTAGCCACA 732

QY 301 TAATGACGACTTAATGTCTTACTGGCAGCTGCACCTTGCATGATGAGTGACAGATGTTTTT 360
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 QY 361 GATAGATCAGCGGCAATATGTTAAATGCAAACTAACTTTTACTATAATGTTGTTCT 420
 DB 793 GATAGATCAGCGGCAATATGTTAAATGCAAACTAACTTTTACTATAATGTTGTTCT 852
 QY 421 CCTTAAGGTGAAGCTCCTGGCGTTTAAAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 DB 853 CCTTAAGGTGAAGCTCCTGGCGTTTAAAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 912
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 DB 1033 CTTGATGATGGAGTGACACTTCTTTTAAATACATCAGCCACATATTGTGTTAAATGACAGA 1092
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 QY 781 ATAAACAAAGAGATTCTCTGCCACTGCAGTGCCTAAGCTAATTTAGCCACATAATGC 840
 DB 1213 ATAAACAAAGAGATTCTCTGCCACTGCAGTGCCTAAGCTAATTTAGCCACATAATGC 1272
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 DB 1273 AGTACTTAATGTTCCAACTGGCACTGCAATTCAGAGGAGTGACACTGTTGTTTGTAGTAAT 1332
 QY 901 TCATCCACATAATGTTCTTAAATGCAATGCTAATTTACTTTTAAATGTTGTTGTTGTTGTTGTT 960
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 QY 961 GGTAAAGTTAATGTTTAAAGTGCAGTAAGTAAACTTCCAGCACATGCTCCAGCT 1020
 DB 1393 GGTAAAGTTAATGTTTAAAGTGCAGTAAGTAAACTTCCAGCACATGCTCCAGCT 1452
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 QY 1141 TTTTTCGATCAAAACAACTGTTTACAGCAGGTGATGATGATGATGATGATGATGATGATGATGATGAT 1200
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 QY 1201 AAAAAATTAATCTTCTGTCGACAGCTAAAGTATATGCTGAAGCTACTCAAAAAGTATAA 1260
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 QY 1321 TTATG 1326
 DB 1753 TTATG 1758

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RESULT 2
ICYMANT      1249 bp      mRNA      linear      INV 18-SEP-1998
LOCUS      Ichthyophthirius multifiliis immobilization antigen precursor,
DEFINITION      mRNA, partial cds.
ACCESSION      M92907.1      GI:3628568
VERSION      M92907.1
KEYWORDS
SOURCE
ORGANISM      Ichthyophthirius multifiliis.
               Ichthyophthirius multifiliis.
               Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
               Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE
AUTHORS      Lin, T. L. and Dickerson, H. W.
TITLE      Purification and partial characterization of immobilization
               antigens from Ichthyophthirius multifiliis
JOURNAL      J. Protozool. 39 (4), 457-463 (1992)
MEDLINE      93020590
PUBMED      1383510
REFERENCE
AUTHORS      Clark, T. G., McGraw, R. A. and Dickerson, H. W.
TITLE      Developmental expression of surface antigen genes in the parasitic
               ciliate Ichthyophthirius multifiliis
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 89 (14), 6363-6367 (1992)
MEDLINE      92335298
PUBMED      1631132
REFERENCE
AUTHORS      Clark, T.
TITLE      Direct Submission
JOURNAL      Submitted (06-JUN-1992) Microbiology and Immunology, Cornell
               University, Ithaca, NY 14853, USA
AUTHORS      Clark, T.
TITLE      Direct Submission
JOURNAL      Submitted (18-SEP-1998) Microbiology and Immunology, Cornell
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REMARK      Sequence update by submitter
COMMENT      On Sep 18, 1998 this sequence version replaced gi:159289.
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QY      656     GCAGACTTAACCTTTTACTATAATGTTGTTCTCCTTAAGGTGAAGCTCCTGCGCTTAAG 715
Db      601     GCAGACTTAACCTTTTACTATAATGTTGTTCTCCTTAAGGTGAAGCTCCTGCGCTTAAG 660

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QY      836     AATGAGTACTTAAATGTCCAACTGGCAGCTGCAATTCAGACGGAGTGACACTTGTGTTTA 895
Db      781     AATGAGTACTTAAATGTCCAACTGGCAGCTGCAATTCAGACGGAGTGACACTTGTGTTTA 840

QY      896     GTAATTTCATCCACATAATGTTCTTAAATGCATTGCTTAATTTACTTTTTTAATGTAATTCG 955
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Db 1141 GTACTAAAAAATACTCTGGTGCCACAGCT 1172
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RESULT 3
AF405431 1520 bp mRNA linear INV 27-FEB-2002
LOCUS Ichthyophthirius multifiliis 52kDa immobilization antigen variant B
DEFINITION protein mRNA, complete cds.
ACCESSION AF405431 GI:15290741
VERSION 1
KEYWORDS
SOURCE
ORGANISM
Ichthyophthirius multifiliis.
Ichthyophthirius multifiliis.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE
1 (bases 1 to 1520)
Lin, Y., Lin, T.L., Wang, C.C., Wang, X., Stieger, K., Klopfleisch, R.
and Clark, T.G.
Variation in primary sequence and tandem repeat copy number among
1-antigens of Ichthyophthirius multifiliis
Mol. Biochem. Parasitol. 120 (1), 93-106 (2002)
21839613
PUBMED 11849709
REFERENCE
2 (bases 1 to 1520)
Lin, Y., Wang, J.C. and Clark, T.C.
Direct Submission
Submitted (03-AUG-2001) Microbiology and Immunology, NYSCVM Cornell
University, Ithaca, NY 14853, USA
JOURNAL
FEATURES
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Matches 971; Conservative 0; Mismatches 343; Indels 78; Gaps 4;
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Db 41 ATGAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAGAGCT 100
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QY 61 GTTCCATGCTGATGGTACTTACACTCAAGCTGATGTAGCTGATGTAGCTGCTGAT 120
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KEYWORDS
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SOURCE
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ORGANISM
    Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
    Hymenostomata; Ophryoglenina; Ichthyophthirius.
    Lin.Y., Lin.T.L., Wang.C.C., Wang.X., Stieger.K., Klopfleisch.R.
    and Clark.T.G.
    Variation in primary sequence and tandem repeat copy number among
    i-antigens of Ichthyophthirius multifiliis
    Mol. Biochem. Parasitol. 120 (1), 93-106 (2002)
    21899613
    11849709
REFERENCE
    1 (bases 1 to 3026)
    Lin.Y., Lin.T.L. and Clark.T.G.
    Direct Submission
    Submitted (27-NOV-2000) Microbiology and Immunology, NYSCVM Cornell
    University, Ithaca, NY 14853, USA
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    CNVACPTGALDGVTDYVRSTECVKRLNPFYNGNNGTFFNPGKSCQPCPAIK
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    NPGNSTLPCPNKRDYGAETAGGATLAKQCNACPDGTAISAGTNVYVILQTECLN
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Best Local Similarity 56.7%; Pred. No. 4.6e-38;
Matches 660; Conservativeness 0; Mismatches 394; Indels 111; Gaps 6;
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Db 1673 GTGTTAATTCAGAAATTAATTTTATATCAAAATCCTCCAAATTTAATGAGGCTGCTA 1732
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Qy 347 TGACAGATGTTTTGATAGATAGCGCGCATATGTTAAATGCAAACTAACTTTTACT 406
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RESULT 7

AC099174/C

LOCUS

DEFINITION

AC099174

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GI:21728909

HTG: HTGS_PHASE1

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 176822)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,

Alsbrooks,S.L., Amaralunga,H.C., Are,J.R., Ayele,M., Banks,T.,

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Williams,G., Williamson,A., Wleczkyk,R., Wooden,S., Worley,K.,

Wu,C., Wu,Y., Wu,F.F., Zhou,J., Zorrilla,S., Nelson,D.,

Weinstock,G. and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 176822)

Worley,K.C.

Direct Submission

Submitted (09-NOV-2001) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 176822)

Worley,K.C.

Direct Submission

Submitted (12-JUL-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On Jul 11, 2002 this sequence version replaced gi:18846108.

----- Genome Center

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GGZV
Center clone name: CH230-9811
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 115453 bases at least Q40
Consensus quality: 125501 bases at least Q30
Consensus quality: 133023 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 77 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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31459: contig of 1364 bp in length
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32924: contig of 1365 bp in length
33024: gap of unknown length
34073: contig of 1049 bp in length
34074: gap of unknown length

AUTHORS
TITLE
JOURNAL

REFERENCE
AUTHORS
TITLE
JOURNAL

McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (15-FEB-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 204259)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (29-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On May 23, 2002 this sequence version replaced gi:18874253.

COMMENT

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BA0155B20
----- Summary Statistics -----
Sequencing vector: M13; 0%
Chemistry: Dye-primer; 100%
Chemistry: Dye-primer; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 198852 bases at least Q40
Consensus quality: 200032 bases at least Q30
Consensus quality: 201011 bases at least Q20
Insert size: 211000; agarose-gel
Insert size: 203242; sum-of-contigs
Quality coverage: 8.38 in Q20 bases; agarose-gel
Quality coverage: 8.78 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 1327 2375: contig of 1049 bp in length
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* 2476 3800: contig of 1325 bp in length
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* 5877 5977: gap of unknown length
* 5977 7870: contig of 1893 bp in length
* 7870 7969: gap of unknown length
* 7969 9641: contig of 1672 bp in length
* 9642 9741: gap of unknown length
* 9742 14703: contig of 4962 bp in length
* 14704 14804: gap of unknown length
* 14804 20620: contig of 5817 bp in length
* 20621 20720: gap of unknown length
* 20721 30389: contig of 9669 bp in length
* 30390 30489: gap of unknown length
* 30490 38838: contig of 8349 bp in length
* 38839 38939: gap of unknown length
* 38939 51520: contig of 12581 bp in length
* 51520 51620: gap of unknown length
* 51620 70098: contig of 18479 bp in length
* 70099 70199: gap of unknown length
* 70199 100940: contig of 30741 bp in length
* 100940 101040: gap of unknown length
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Location/Qualifiers

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Qy 591 TGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 650
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Db 180259 TGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180318
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Db 180319 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180378
Qy 831 CACATAATGCAGTACTTAATGTCCAACTGCAATTTCAAGACGGGACTGACACTTGT 890

